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                   Substance-Based Searching
 NEWS  3  NOV 24   Search an additional 46,850 records with MEDLINE
                   backfile extension to 1946
 NEWS  4  DEC 14   New PNK Field Allows More Precise Crossover among STN
                   Patent Databases
 NEWS  5  DEC 18   ReaxysFile available on STN
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                   Medicine Patents in CAplus
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                   other enhancements improve searching in STN reload of
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 NEWS 11  JAN 28   CABA will be updated weekly
 NEWS 12  FEB 23   PCTFULL file on STN completely reloaded
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 NEWS 14  FEB 25   LPCI will be replaced by LDPCI
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 NEWS 16  APR 26   Expanded Swedish Patent Application Coverage in CA/CAplus
                   Provides More Current and Complete Information
 NEWS 17  APR 28   The DWPI (files WPINDEX, WPIDS and WPIX) on STN have been
                   enhanced with thesauri for the European Patent Classifications
 NEWS 18  MAY 02   MEDLINE Improvements Provide Fast and Simple Access to DOI and
                   Chemical Name Information
 NEWS 19  MAY 12   European Patent Classification thesauri added to the INPADOC
                   files, PCTFULL, GBFULL and FRFULL
 NEWS 20  MAY 20   PATDPA database updates to end in June 2011
 NEWS 21  MAY 23   Enhanced performance of STN biosequence searches
 NEWS 22  MAY 23   Free Trial of the Numeric Property Search Feature
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=> File MEDLINE, SCISEARCH, LIFESCI, BIOSIS, EMBASE, HCAPLUS, NTIS, ESBIOBASE,
BIOTECHNO, WPIDS, BIOENG, DISSABS
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=> S (substrate) (6A) modeling
L1   4968 (SUBSTRATE) (6A) MODELING

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=> S (protease or proteinase or peptidase) (6A) (crystal structure)
L2        3207 (PROTEASE OR PROTEINASE OR PEPTIDASE) (6A) (CRYSTAL STRUCTURE)

=> s l1 and l2
L3           18 L1 AND L2

=> s l1 (50A) l2
L4            2 L1 (50A) L2

=> duplicate
ENTER REMOVE, IDENTIFY, ONLY, OR (?):remove
ENTER L# LIST OR (END):l4
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L5             2 DUPLICATE REMOVE L4 (0 DUPLICATES REMOVED)

=> d l5 1-2 bib ab

L5   ANSWER 1 OF 2  HCAPLUS  COPYRIGHT 2011 ACS on STN
AN   2009:1563749  HCAPLUS
DN   152:138505
TI   Dengue virus NS3 serine protease. Crystal structure and insights into
     interaction of the active site with substrates by molecular modeling and
     structural analysis of mutational effects. [Retraction of document cited
     in CA130:278575]
AU   Murthy, H. M. Krishna; Clum, S.; Padmanabhan, R.
CS   Fels Institute, Temple University, Philadelphia, PA, 19140, USA
SO   Journal of Biological Chemistry (2009), 284(49), 34468
     CODEN: JBCHA3; ISSN: 0021-9258
PB   American Society for Biochemistry and Molecular Biology
DT   Journal
LA   English
AB   This article has been retracted at the request of the Publisher.

L5   ANSWER 2 OF 2  HCAPLUS  COPYRIGHT 2011 ACS on STN
AN   1999:152913  HCAPLUS
DN   130:278575
TI   Dengue virus NS3 serine protease. Crystal structure and insights into
     interaction of the active site with substrates by molecular modeling and
     structural analysis of mutational effects
AU   Murthy, H. M. Krishna; Clum, S.; Padmanabhan, R.
CS   Fels Institute, Temple University, Philadelphia, PA, 19140, USA
SO   Journal of Biological Chemistry (1999), 274(9), 5573-5580
     CODEN: JBCHA3; ISSN: 0021-9258
PB   American Society for Biochemistry and Molecular Biology
DT   Journal
LA   English
AB   The mosquito-borne dengue viruses are widespread human pathogens causing
     dengue fever, dengue hemorrhagic fever, and dengue shock syndrome, placing
     40% of the world's population at risk with no effective treatment.  The
     viral genome is a pos. strand RNA that encodes a single polyprotein
     precursor.  Processing of the polyprotein precursor into mature proteins
     is carried out by the host signal peptidase and by NS3 serine protease,
     which requires NS2B as a cofactor.  We report here the crystal structure
     of the NS3 serine protease domain at 2.1 A resolution  This structure of the
     protease combined with modeling of peptide substrates into the active site
     suggests identities of residues involved in substrate recognition as well
     as providing a structural basis for several mutational effects on enzyme
     activity.  This structure will be useful for development of specific
     inhibitors as therapeutics against dengue and other flaviviral proteases.
OSC.G   79    THERE ARE 79 CAPLUS RECORDS THAT CITE THIS RECORD (80 CITINGS)
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RE.CNT 73 THERE ARE 73 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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PROCESSING COMPLETED FOR L3
L6 11 DUPLICATE REMOVE L3 (7 DUPLICATES REMOVED)

=> d l6 1-11 bib ab

L6 ANSWER 1 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 2009:1563749 HCAPLUS
DN 152:138505
TI Dengue virus NS3 serine protease. Crystal structure and insights into interaction of the active site with substrates by molecular modeling and structural analysis of mutational effects. [Retraction of document cited in CA130:278575]
AU Murthy, H. M. Krishna; Clum, S.; Padmanabhan, R.
CS Fels Institute, Temple University, Philadelphia, PA, 19140, USA
SO Journal of Biological Chemistry (2009), 284(49), 34468
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB This article has been retracted at the request of the Publisher.

L6 ANSWER 2 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 2008:571683 HCAPLUS
DN 149:121716
TI Enzymatic Activity of the Staphylococcus aureus SplB Serine Protease is Induced by Substrates Containing the Sequence Trp-Glu-Leu-Gln
AU Dubin, Grzegorz; Stec-Niemczyk, Justyna; Kisielewska, Magdalena; Pustelny, Katarzyna; Popowicz, Grzegorz M.; Bista, Michal; Kantyka, Tomasz; Boulware, Kevin T.; Stennicke, Henning R.; Czarna, Anna; Phopaisarn, Mullika; Daugherty, Patrick S.; Thogersen, Ida B.; Enghild, Jan J.; Thornberry, Nancy; Dubin, Adam; Potempa, Jan
CS Department of Microbiology, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Gronostajowa 7, Krakow, 30-387, Pol.
SO Journal of Molecular Biology (2008), 379(2), 343-356
CODEN: JMOBAK; ISSN: 0022-2836
PB Elsevier Ltd.
DT Journal
LA English
AB Proteases are of significant importance for the virulence of Staphylococcus aureus. Nevertheless, their subset, the serine protease-like proteins, remains poorly characterized. Here presented is an investigation of SplB protease catalytic activity revealing that the enzyme possesses exquisite specificity and only cleaves efficiently after the sequence Trp-Glu-Leu-Gln. To understand the mol. basis for such selectivity, we solved the three-dimensional structure of SplB to 1.8 Å. Modeling of substrate binding to the protease demonstrated that selectivity relies in part on a canonical specificity pockets-based mechanism. Significantly, the conformation of residues that ordinarily form the oxyanion hole, an essential structural element of the catalytic machinery of serine proteases, is not canonical in the SplB structure. We

postulate that within SplB, the oxyanion hole is only formed upon docking of a substrate containing the consensus sequence motif. It is suggested that this unusual activation mechanism is used in parallel with classical determinants to further limit enzyme specificity. Finally, to guide future development, we attempt to point at likely physiol. substrates and thus the role of SplB in staphylococcal physiol.

OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 11 MEDLINE on STN DUPLICATE 1
AN 2007031116 MEDLINE
DN PubMed ID: 17210913
TI The crystal structure of the rhomboid peptidase from Haemophilus influenzae provides insight into intramembrane proteolysis.
AU Lemieux M Joanne; Fischer Sarah J; Cherney Maia M; Bateman Katherine S; James Michael N G
CS Group in Protein Structure and Function, Department of Biochemistry, University of Alberta, Edmonton, AB, Canada T6G 2H7.
SO Proceedings of the National Academy of Sciences of the United States of America, (2007 Jan 16) Vol. 104, No. 3, pp. 750-4. Electronic Publication: 2007-01-08.
Journal code: 7505876. ISSN: 0027-8424. L-ISSN: 0027-8424.
Report No.: NLM-PMC1783385.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
OS PDB-2NR9
EM 200702
ED Entered STN: 18 Jan 2007
Last Updated on STN: 28 Feb 2007
Entered Medline: 27 Feb 2007
OSC.G 19 There are 19 MEDLINE records that cite this record
REM.CNT 25 There are 25 cited references available in MEDLINE for this document.
AB Rhomboid peptidases are members of a family of regulated intramembrane peptidases that cleave the transmembrane segments of integral membrane proteins. Rhomboid peptidases have been shown to play a major role in developmental processes in Drosophila and in mitochondrial maintenance in yeast. Most recently, the function of rhomboid peptidases has been directly linked to apoptosis. We have solved the structure of the rhomboid peptidase from Haemophilus influenzae (hiGlpG) to 2.2-A resolution. The phasing for the crystals of hiGlpG was provided mainly by molecular replacement, by using the coordinates of the Escherichia coli rhomboid (ecGlpG). The structural results on these rhomboid peptidases have allowed us to speculate on the catalytic mechanism of substrate cleavage in a membranous environment. We have identified the relative disposition of the nucleophilic serine to the general base/acid function of the conserved histidine. Modeling a tetrapeptide substrate in the context of the rhomboid structure reveals an oxyanion hole comprising the side chain of a second conserved histidine and the main-chain NH of the nucleophilic serine residue. In both hiGlpG and ecGlpG structures, a water molecule occupies this oxyanion hole.

L6 ANSWER 4 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 2006:397830 HCAPLUS
DN 145:39879

TI Substrate envelope and drug resistance: crystal structure of RO1 in complex with wild-type human immunodeficiency virus type 1 protease
AU Prabu-Jeyabalan, Moses; King, Nancy M.; Nalivaika, Ellen A.; Heilek-Snyder, Gabrielle; Cammack, Nick; Schiffer, Celia A.
CS Department of Biochemistry & Molecular Pharmacology, University of Massachusetts Medical School, Worcester, MA, 01605, USA
SO Antimicrobial Agents and Chemotherapy (2006), 50(4), 1518-1521
CODEN: AMACCQ; ISSN: 0066-4804
PB American Society for Microbiology
DT Journal
LA English
AB In our previous crystallog. studies of human immunodeficiency virus type 1 (HIV-1) protease-substrate complexes, the authors described a conserved "envelope" that appears to be important for substrate recognition and the selection of drug-resistant mutations. In this study, the complex of HIV-1 protease with the inhibitor RO1 was determined and comparison with the substrate envelope provides a rationale for mutational patterns.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 2005:490422 HCAPLUS
DN 143:55635
TI Cloning, sequence and mutagenesis of Asp serine proteinase from Cellulomonas and use of variant Asp in detergents, feed and textile processing
IN Jones, Brian Edward; Kolkman, Marc; Leeflang, Chris; Oh, Hiroshi; Poulose, Ayrookaran J.; Sadlowski, Eugene S.; Shaw, Andrew; Van der Kleij, Wilhelmus A. H.; Van Marrewijk, Leo
PA Genencor International, Inc., USA; The Procter & Gamble Company
SO PCT Int. Appl., 356 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2005052146	A2	20050609	WO 2004-US39066	20041119
	WO 2005052146	A3	20051110		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
	RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2004293826	A1	20050609	AU 2004-293826	20041119
	AU 2004293826	B2	20090917		
	CA 2546451	A1	20050609	CA 2004-2546451	20041119
	EP 1694847	A2	20060830	EP 2004-811731	20041119
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK, IS				
	CN 1906303	A	20070131	CN 2004-80040520	20041119
	BR 2004016797	A	20070417	BR 2004-16797	20041119

	JP 2007515164	T	20070614	JP 2006-541585	20041119
	MX 2006005107	A	20060714	MX 2006-5107	20060504
	IN 2006DN02866	A	20070810	IN 2006-DN2866	20060519
	KR 2006121212	A	20061128	KR 2006-7012183	20060619
	US 20080063774	A1	20080313	US 2007-809104	20070531
	AU 2009250976	A1	20100114	AU 2009-250976	20091216
PRAI	US 2003-523609P	P	20031119		
	AU 2004-293826	A3	20041119		
	WO 2004-US39066	W	20041119		
	US 2006-576331	A2	20060418		
	US 2006-583334	A1	20061019		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention provides novel serine proteases, novel genetic material encoding these enzymes, and proteolytic proteins obtained from Micrococcineae spp., including but not limited to Cellulomonas spp. and variant proteins developed therefrom. In particular, the present invention provides serine protease compns. obtained from a Cellulomonas spp., DNA encoding the serine protease, vectors comprising the DNA encoding the serine protease, host cells transformed with the vector DNA, and an enzyme produced by the host cells. The nucleotide sequence of the gene asp and the encoded amino acid sequence of the Asp serine protease from Cellulomonas strain 69B4 are disclosed. The crystal structure and the atomic coordinates of the Asp serine protease from Cellulomonas 69B4 are provided. The nucleotide sequences and the encoded amino acid sequences of homologous serine proteases from Cellulomonas spp. and related microorganisms are also provided. The present invention also provides cleaning compns. (e.g., detergent compns.), animal feed compns., and textile and leather processing compns. comprising protease(s) obtained from a Micrococcineae spp., including but not limited to Cellulomonas spp. In alternative embodiments, the present invention provides mutant (i.e., variant) proteases derived from the wild-type proteases described herein. These mutant proteases also find use in numerous applications.

OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L6 ANSWER 6 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN

AN 2006:523285 HCAPLUS

DN 144:463170

TI Design of wide-spectrum inhibitors targeting Coronavirus main proteases. [Erratum to document cited in CA144:427824]

AU Yang, Haitao; Xie, Weiqing; Xue, Xiaoyu; Yang, Kailin; Ma, Jing; Liang, Wenxue; Qi, Zzhao; Zhou, Zhe; Pei, Duanqing; Ziebuhr, John; Hilgenfeld, Rolf; Yuen, Kwok Yung; Wong, Luet; Gao, Guangxia; Chen, Saijuan; Chen, Zhu; Ma, Dawei; Bartlam, Mark; Rao, Zihe

CS Tsinghua-IBP Joint Research Group for Structural Biology, Tsinghua University, Beijing, Peop. Rep. China

SO PLoS Biology (2005), 3(11), 2044
CODEN: PBLIBG; ISSN: 1545-7885

PB Public Library of Science

DT Journal; (online computer file)

LA English

AB There is an error in equation 1, despite the Note Added in Proof indicating that the equation has been corrected The second reaction step should not have a reverse arrow. The correct equation is given.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L6 ANSWER 7 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN

AN 2005:1131448 HCAPLUS

DN 144:427824

TI Design of wide-spectrum inhibitors targeting Coronavirus main proteases

AU Yang, Haitao; Xie, Weiqing; Xue, Xiaoyu; Yang, Kailin; Ma, Jing; Liang, Wenxue; Zhao, Qi; Zhou, Zhe; Pei, Duanqing; Ziebuhr, John; Hilgenfeld, Rolf; Yuen, Kwok Yung; Wong, Luet; Gao, Guangxia; Chen, Saijuan; Chen, Zhu; Ma, Dawei; Bartlam, Mark; Rao, Zihe
CS Tsinghua-IBP Joint Research Group for Structural Biology, Tsinghua University, Beijing, Peop. Rep. China
SO PLoS Biology (2005), 3(10), 1742-1752
CODEN: PBLIBG; ISSN: 1545-7885
URL: http://biology.plosjournals.org/archive/1545-7885/3/10/pdf/10.1371_1545-7885_3_10_complete.pdf
PB Public Library of Science
DT Journal; (online computer file)
LA English
OS CASREACT 144:427824
AB The genus Coronavirus contains about 25 species of coronaviruses (CoVs), which are important pathogens causing highly prevalent diseases and often severe or fatal in humans and animals. No licensed specific drugs are available to prevent their infection. Different host receptors for cellular entry, poorly conserved structural proteins (antigens), and the high mutation and recombination rates of CoVs pose a significant problem in the development of wide-spectrum anti-CoV drugs and vaccines. CoV main proteases (Mpros), which are key enzymes in viral gene expression and replication, were revealed to share a highly conservative substrate-recognition pocket by comparison of four crystal structures and a homol. model representing all three genetic clusters of the genus Coronavirus. This conclusion was further supported by enzyme activity assays. Mechanism-based irreversible inhibitors were designed, based on this conserved structural region, and a uniform inhibition mechanism was elucidated from the structures of Mpro-inhibitor complexes from severe acute respiratory syndrome-CoV and porcine transmissible gastroenteritis virus. A structure-assisted optimization program has yielded compds. with fast in vitro inactivation of multiple CoV Mpros, potent antiviral activity, and extremely low cellular toxicity in cell-based assays. Further modification could rapidly lead to the discovery of a single agent with clin. potential against existing and possible future emerging CoV-related diseases.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 11 BIOSIS COPYRIGHT (c) 2011 The Thomson Corporation on STN DUPLICATE 2
AN 1999:153674 BIOSIS
DN PREV199900153674
TI Dengue virus NS3 serine protease: Crystal structure and insights into interaction of the active site with substrates by molecular modeling and structural analysis of mutational effects.
AU Murthy, H. M. Krishna [Reprint author]; Clum, S.; Padmanabhan, R.
CS CMC, Univ. Alabama Birmingham, 79-THT, MCLM-248, 1918 University Blvd., Birmingham, AL 35294-0005, USA
SO Journal of Biological Chemistry, (Feb. 26, 1999) Vol. 274, No. 9, pp. 5573-5580. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 16 Apr 1999
Last Updated on STN: 16 Apr 1999
AB The mosquito-borne dengue viruses are widespread human pathogens causing dengue fever, dengue hemorrhagic fever, and dengue shock syndrome, placing 40% of the world's population at risk with no effective treatment. The viral genome is a positive strand RNA that encodes a single polyprotein

precursor. Processing of the polyprotein precursor into mature proteins is carried out by the host signal peptidase and by NS3 serine protease, which requires NS2B as a cofactor. We report here the crystal structure of the NS3 serine protease domain at 2.1 ANG resolution. This structure of the protease combined with modeling of peptide substrates into the active site suggests identities of residues involved in substrate recognition as well as providing a structural basis for several mutational effects on enzyme activity. This structure will be useful for development of specific inhibitors as therapeutics against dengue and other flaviviral proteases.

L6 ANSWER 9 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:714506 HCAPLUS
DN 132:10359
TI The structure of the 2A proteinase from a common cold virus: a proteinase responsible for the shut-off of host-cell protein synthesis
AU Petersen, Jens F. W.; Cherney, Maia M.; Liebig, Hans-Dieter; Skern, Tim; Kuechler, Ernst; James, Michael N. G.
CS MRC Group in Protein Structure and Function, Department of Biochemistry, University of Alberta, Edmonton, AB, T6G 2H7, Can.
SO EMBO Journal (1999), 18(20), 5463-5475
CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English
AB The crystal structure of 2A proteinase (picornain 2A; EC 3.4.22.29) from human rhinovirus serotype 2 (HRV2-2Apro) was solved to 1.95 Å resolution The structure had an unusual, although chymotrypsin-related, fold comprising a unique 4-stranded β-sheet as the N-terminal domain and a 6-stranded β-barrel as the C-terminal domain. A tightly bound Zn(II) ion, essential for the stability of HRV2-2Apro, was tetrahedrally coordinated by 3 Cys S atoms and 1 His N atom. The active site consisted of a catalytic triad formed by His-18, Asp-35 and Cys-106. Asp-35 was addnl. involved in an extensive H-bonding network. Modeling studies revealed a substrate-induced fit that explained the specificity of subsites S4, S2, S1, and S1'. The structure of HRV2-2Apro suggested the mechanism of the cis cleavage and its release from the polyprotein.
OSC.G 59 THERE ARE 59 CAPLUS RECORDS THAT CITE THIS RECORD (59 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 11 BIOSIS COPYRIGHT (c) 2011 The Thomson Corporation on STN
AN 1991:226794 BIOSIS
DN PREV199191118254; BA91:118254
TI A RANGE OF CATALYTIC EFFICIENCIES WITH AVIAN RETROVIRAL PROTEASE SUBUNITS GENETICALLY LINKED TO FORM SINGLE POLYPEPTIDE CHAINS.
AU BIZUB D [Reprint author]; WEBER I T; CAMERON C E; LEIS J P; SKALKA A M
CS FOX CHASE CANCER CENT, INST CANCER RES, 7701 BURKHOLME AVE, PHILADELPHIA, PA 19111, USA
SO Journal of Biological Chemistry, (1991) Vol. 266, No. 8, pp. 4951-4958.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 9 May 1991
Last Updated on STN: 10 May 1991
AB Molecular modeling based on the crystal structure of the Rous sarcoma virus (RSV) protease dimer has been used to link the two identical subunits of this enzyme into a functional, single polypeptide chain resembling the nonviral aspartic protease. Six different linkages were

selected to test the importance of different interactions between the amino acids at the amino and carboxyl termini of the two subunits. These linkages were introduced into molecular clones of fused protease genes and the linked protease dimers were expressed in Escherichia coli and purified. Catalytically active proteins were obtained from the inclusion body fraction after renaturation. The linked protease dimers exhibited a 10-20-fold range in catalytic efficiencies (Vmax/Km) on peptide substrates. Both flexibility and ionic interactions in the linkage region affect catalytic efficiency. Some of the linked protease dimers were 2-3-fold more active than the nonlinked enzyme purified from bacteria, although substrate specifities were unchanged. Similar relative efficiencies were observed using a polyprotein precursor as substrate. Mutation of one catalytic Asp in the most active linked protease dimer inactivated the enzyme, demonstrating that these proteins function as single polypeptide chains rather than as multimers.

L6 ANSWER 11 OF 11 HCAPLUS COPYRIGHT 2011 ACS on STN
AN 1992:2832 HCAPLUS
DN 116:2832
OREF 116:567a,570a
TI Modeling of structure of human immunodeficiency virus-1 protease with substrate based on crystal structure of Rous sarcoma virus protease
AU Weber, Irene T.
CS Dep. Pharmacol., Thomas Jefferson Univ., Philadelphia, PA, 19107, USA
SO Methods in Enzymology (1991), 202(Mol. Des. Model.: Concepts Appl., Pt. A), 727-41
CODEN: MENZAU; ISSN: 0076-6879
DT Journal
LA English
AB The conformation and subunit structure of HIV-1 virus aspartic proteinase-substrate complex were derived from the crystal structure of Rous sarcoma virus proteinase.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

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